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Virology 350 (2006) 501–502

VIROLOGY

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Corrigendum

Corrigendum to "The complete genomic sequence of the modified vaccinia Ankara (MVA) strain: Comparison with other orthopoxviruses" [Virology 244 (1998) 365–396]

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Available online 5 June 2006

The authors would like to correct some sequencing errors that appeared in their original paper, referenced above.

The sequence of a second MVA isolate with a different passage history was submitted to GenBank (accession number AY603355; Esposito, J.J., Frace, M., Sammons, S.A., Olsen-Rasmussen, M.S., Osborne, J., Khristova, M. and Wohlhueter, R.M., 2004. Vaccinia virus strain Acambis 3000 modified virus Ankara (MVA), complete genome). A comparison of the earlier deposited sequence of the MVAII/85 derived MVA M4 clone (accession number U94848; above-referenced article) with the new sequence (AY603355) revealed five single nucleotide differences in the viral genome (Table 1). A review of our raw sequence data suggested that sequencing errors, rather than genetic variation, may have resulted in the five single nucleotide differences in the U94848 sequence. Therefore, the five differing regions in the MVA M4 clone were re-sequenced using the improved dye terminators now available. We found that the five differences in the original data resulted from errors in the original sequencing experiments. When the corrected MVA M4 sequences were compared to the AY603355 GenBank entry, no differences were found (Table 1). Thus, the AY603355 sequence (Esposito et al., 2004) and the U94848 sequence (Antoine et al., 1998) are identical in their coding regions. This sequence identity indicates that MVA is extremely stable in chicken cells. The stability of the nearly 170-kb total genome is remarkable in light of the current development of MVA as a safe next-generation smallpox vaccine and a vector for recombinant vaccines.

DOI of original article: 10.1016/j.virol.1998.9123.

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doi:10.1016/j.virol.2006.04.025

Table 1
Nucleotide positions differing in the two MVA sequences

	AccNo [a]/position	Sequence	Primers used for PCR and sequencing
		x	
1	U94848/68740	TTTGGTCATAATAGAATGTA	5#-CACTTGGTAGTTGAATCTACCTA-3′
	AY603355/62950	TTTGGTCATGATAGAATGTA	5#-CTGATGGAGCTGTGACTAGTC-3′
	Re-seq. MVA-M4 [b]	TTTGGTCATGATAGAATGTA	
		x	
2	U94848/73886	GGTATATTTCTATCACCTCG	5#-GGAGATAGATATCCGTCATTGCA-3′
	AY603355/68096	GGTATATTTTTATCACCTCG	5#-CTAGCAGTAGACTCATTTAGAGA-3′
	Re-seq. MVA-M4	GGTATATTTTTATCACCTCG	
		x	
3	U94848/108489	AGATGGCGGCGTCGTCGTCT	5#-GCGTATACTCCCTTGCATCATA-3′
	AY603355/102699	AGATGGCGGTGTCGTCGTCT	5#-CTCTACACCAAAGTCGTCAATCT-3′
	Re-seq. MVA-M4	AGATGGCGGTGTCGTCGTCT	
		x	
4	U94848/114308	CAATGCCATTTTACACGATG	5#-CATCATCAAAAGAGACAGAGTCAC-3′
	AY603355/108518	CAATGCCATCTTACACGATG	5#-ATCTGTGACTCGGAACCG-3′
	Re-seq. MVA-M4	CAATGCCATCTTACACGATG	
		x	
5	U94848/114945	TTAGTTACTCTTGGTCTAAT	5#-GTTTCTATACTGTCTGTAACTCTG-3′
	AY603355/109155	TTAGTTACTTTTGGTCTAAT	5#-CTGAGACAGGATTCATGAGATTC-3′
	Re-seq. MVA-M4	TTAGTTACTTTTGGTCTAAT	

Note. The marked position (x, bold type) indicates the sequence error in the U94848 sequence.

[a] GenBank accession number; x, positions of differing nucleotides.

[b] PCR products of strand and counterstrand of the five regions were sequenced directly with MVA-M4 DNA (M4-MVA, 13.03.97; ID: 10381 0772_0773) as a template.